

SEQUENCE SUBMISSION

5 SEQ ID NO: 1 is a primate HDTEA84 nucleic acid sequence.
SEQ ID NO: 2 is a primate HDTEA84 amino acid sequence.
10 SEQ ID NO: 3 is a primate HSLJD37R nucleic acid sequence.
SEQ ID NO: 4 is a primate HSLJD37R amino acid sequence.
SEQ ID NO: 5 is supplemented primate HSLJD37R nucleic acid sequence.
SEQ ID NO: 6 is supplemented primate HSLJD37R amino acid sequence.
15 SEQ ID NO: 7 is variant primate HSLJD37R nucleic acid sequence.
SEQ ID NO: 8 is variant primate HSLJD37R amino acid sequence.
SEQ ID NO: 9 is murine TNF-R2 amino acid sequence.
SEQ ID NO: 10 is human TNF-R2 amino acid sequence.
SEQ ID NO: 11 is human OPG amino acid sequence.
20 SEQ ID NO: 12 is a rodent RANKL nucleic acid sequence.
15 SEQ ID NO: 13 is a rodent RANKL amino acid sequence.
SEQ ID NO: 14 is a primate RANKL nucleic acid sequence.
SEQ ID NO: 15 is a primate RANKL amino acid sequence.
SEQ ID NO: 16 is another primate RANKL nucleic acid sequence.
SEQ ID NO: 17 is another primate RANKL amino acid sequence.
25 SEQ ID NO: 18 is a variant primate RANKL nucleic acid sequence.
SEQ ID NO: 19 is a variant primate RANKL amino acid sequence.

<110> Murphy, Erin E.
Mattson, Jeanine D.
25 Bates, Elizabeth Esther Mary
Gorman, Daniel M.
Lebecque, Serge J.E.

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	Leu Met Glu Asp Thr Thr Gln Leu Glu Thr Asp Lys Leu Ala Leu Pro			
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	Asp Ser Thr Ser Ser Gly Ser Ser Ala Leu Ser Arg Asn Gly Ser Phe			
25	520	525	530	535
	Ile Thr Lys Glu Lys Lys Asp Thr Val Leu Arg Gln Val Arg Leu Asp			
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	555	560	565	
	Pro Glu Glu Leu Arg Val Ile Glu Glu Ile Pro Gln Ala Glu Asp Lys			
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	Leu Asp Arg Leu Phe Glu Ile Ile Gly Val Lys Ser Gln Glu Ala Ser			
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	Leu Thr Cys Asp Lys Cys Pro Ala Gly Thr Tyr Val Ser Glu His Cys	
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	Thr Asn Thr Ser Leu Arg Val Cys Ser Ser Cys Pro Val Gly Thr Phe	
	40 45 50 55	
25	acc agg cat gag aat ggc ata gag aaa tgc cat gac tgt agt cag cca	336
	Thr Arg His Glu Asn Gly Ile Glu Lys Cys His Asp Cys Ser Gln Pro	
	60 65 70	
30	tgc cca tgg cca atg att gag aaa tta cct tgt gct gcc ttg act gac	384
	Cys Pro Trp Pro Met Ile Glu Lys Leu Pro Cys Ala Ala Leu Thr Asp	
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	Arg Glu Cys Thr Cys Pro Pro Gly Met Phe Gln Ser Asn Ala Thr Cys	
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40	gcc ccc cat acg gtg tgt cct gtg ggt tgg ggt gtg cgg aag aaa ggg	480
	Ala Pro His Thr Val Cys Pro Val Gly Trp Gly Val Arg Lys Lys Gly	
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45	aca gag act gag gat gtg cgg tgt aag cag tgt gct cgg ggt acc ttc	528
	Thr Glu Thr Glu Asp Val Arg Cys Lys Gln Cys Ala Arg Gly Thr Phe	
	120 125 130 135	
50	tca gat gtg cct tct agt gtg atg aaa tgc aaa gca tac aca gac tgt	576
	Ser Asp Val Pro Ser Ser Val Met Lys Cys Lys Ala Tyr Thr Asp Cys	
	140 145 150	
55	ctg agt cag aac ctg gtg gtg atc aag ccg ggg acc aag gag aca gac	624
	Leu Ser Gln Asn Leu Val Val Ile Lys Pro Gly Thr Lys Glu Thr Asp	
	155 160 165	
60	aac gtc tgt ggc aca ctc ccg tcc ttc tcc agc tcc acc tca cct tcc	672
	Asn Val Cys Gly Thr Leu Pro Ser Phe Ser Ser Ser Thr Ser Pro Ser	
	170 175 180	
65	cct ggc aca gcc atc ttt cca cgc cct gag cac atg gaa acc cat gaa	720
	Pro Gly Thr Ala Ile Phe Pro Arg Pro Glu His Met Glu Thr His Glu	
	185 190 195	
70	gtc cct tcc tcc act tat gtt ccc aaa ggc atg aac tca aca gaa tcc	768
	Val Pro Ser Ser Thr Tyr Val Pro Lys Gly Met Asn Ser Thr Glu Ser	
	200 205 210 215	

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	Asn Ser Ser Ala Ser Val Arg Pro Lys Val Leu Ser Ser Ile Gln Glu	
	220 225 230	
5	ggg aca gtc cct gac aac aca agc tca gca agg ggg aag gaa gac gtg	864
	Gly Thr Val Pro Asp Asn Thr Ser Ser Ala Arg Gly Lys Glu Asp Val	
	235 240 245	
10	aac aag acc ctc cca aac ctt cag gta gtc aac cac cag caa ggc ccc	912
	Asn Lys Thr Leu Pro Asn Leu Gln Val Val Asn His Gln Gln Gly Pro	
	250 255 260	
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	His His Arg His Ile Leu Lys Leu Leu Pro Ser Met Glu Ala Thr Gly	
	265 270 275	
20	ggc gag aag tcc agc acg ccc atc aag ggc ccc aag agg gga cat cct	1008
	Gly Glu Lys Ser Ser Thr Pro Ile Lys Gly Pro Lys Arg Gly His Pro	
	280 285 290 295	
	aga cag aac cta cac aag cat ttt gac atc aat gag cat ttg ccc tgg	1056
	Arg Gln Asn Leu His Lys His Phe Asp Ile Asn Glu His Leu Pro Trp	
	300 305 310	
25	atg att gtg ctt ttc ctg ctg ctg gtg ctt gtg gtg att gtg gtg tgc	1104
	Met Ile Val Leu Phe Leu Leu Leu Val Leu Val Val Ile Val Val Cys	
	315 320 325	
30	agt atc cgg aaa agc tcg agg act ctg aaa aag ggg ccc cgg cag gat	1152
	Ser Ile Arg Lys Ser Ser Arg Thr Leu Lys Lys Gly Pro Arg Gln Asp	
	330 335 340	
35	ccc agt gcc att gtg gaa aag gca ggg ctg aag aaa tcc atg act cca	1200
	Pro Ser Ala Ile Val Glu Lys Ala Gly Leu Lys Lys Ser Met Thr Pro	
	345 350 355	
40	acc cag aac cgg gag aaa tgg atc tac tac tgc aat ggc cat gga ccc	1248
	Thr Gln Asn Arg Glu Lys Trp Ile Tyr Tyr Cys Asn Gly His Gly Pro	
	360 365 370 375	
	cat gat gag gag tgg ggg ttg atg gag aga cat att caa gat att tat	1296
	His Asp Glu Glu Trp Gly Leu Met Glu Arg His Ile Gln Asp Ile Tyr	
	380 385 390	
45	att caa aga agc aat caa gat tca gaa aga tgg ggt tgataatttt	1342
	Ile Gln Arg Ser Asn Gln Asp Ser Glu Arg Trp Gly	
	395 400	
50	tacttcaccc tgggaggcag catagtgcag tgaaaggtat cgatatcctg aagcttgtag	1402
	cagcccaagt gggaagccag tggaagata tctatcagtt tctttgcaat gccagtgaga	1462
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-5 -1 1 5

10 Asn Leu Ile Gly Thr Tyr Arg His Val Asp Arg Ala Thr Gly Gln Val
10 15 20

Leu Thr Cys Asp Lys Cys Pro Ala Gly Thr Tyr Val Ser Glu His Cys
15 25 30 35

Thr Asn Thr Ser Leu Arg Val Cys Ser Ser Cys Pro Val Gly Thr Phe
40 45 50 55

20 Thr Arg His Glu Asn Gly Ile Glu Lys Cys His Asp Cys Ser Gln Pro
60 65 70

Cys Pro Trp Pro Met Ile Glu Lys Leu Pro Cys Ala Ala Leu Thr Asp
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25 Arg Glu Cys Thr Cys Pro Pro Gly Met Phe Gln Ser Asn Ala Thr Cys
90 95 100

Ala Pro His Thr Val Cys Pro Val Gly Trp Gly Val Arg Lys Lys Gly
105 110 115

Thr Glu Thr Glu Asp Val Arg Cys Lys Gln Cys Ala Arg Gly Thr Phe
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35 Ser Asp Val Pro Ser Ser Val Met Lys Cys Lys Ala Tyr Thr Asp Cys
140 145 150

Leu Ser Gln Asn Leu Val Val Ile Lys Pro Gly Thr Lys Glu Thr Asp
155 160 165

40 Asn Val Cys Gly Thr Leu Pro Ser Phe Ser Ser Ser Thr Ser Pro Ser
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Pro Gly Thr Ala Ile Phe Pro Arg Pro Glu His Met Glu Thr His Glu
185 190 195

Val Pro Ser Ser Thr Tyr Val Pro Lys Gly Met Asn Ser Thr Glu Ser
200 205 210 215

50 Asn Ser Ser Ala Ser Val Arg Pro Lys Val Leu Ser Ser Ile Gln Glu
220 225 230

Gly Thr Val Pro Asp Asn Thr Ser Ser Ala Arg Gly Lys Glu Asp Val
235 240 245

55 Asn Lys Thr Leu Pro Asn Leu Gln Val Val Asn His Gln Gln Gly Pro
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His His Arg His Ile Leu Lys Leu Leu Pro Ser Met Glu Ala Thr Gly
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Gly Glu Lys Ser Ser Thr Pro Ile Lys Gly Pro Lys Arg Gly His Pro
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 5 Arg Gln Asn Leu His Lys His Phe Asp Ile Asn Glu His Leu Pro Trp
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 Met Ile Val Leu Phe Leu Leu Leu Val Leu Val Val Ile Val Val Cys
 315 320 325
 10 Ser Ile Arg Lys Ser Ser Arg Thr Leu Lys Lys Gly Pro Arg Gln Asp
 330 335 340
 Pro Ser Ala Ile Val Glu Lys Ala Gly Leu Lys Lys Ser Met Thr Pro
 345 350 355
 Thr Gln Asn Arg Glu Lys Trp Ile Tyr Tyr Cys Asn Gly His Gly Pro
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 20 His Asp Glu Glu Trp Gly Leu Met Glu Arg His Ile Gln Asp Ile Tyr
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 35 40 45
 Arg Lys Ala Gln Met Cys Cys Ala Lys Cys Pro Pro Gly Gln Tyr Val
 50 55 60
 45 Lys His Phe Cys Asn Lys Thr Ser Asp Thr Val Cys Ala Asp Cys Glu
 65 70 75 80
 Ala Ser Met Tyr Thr Gln Val Trp Asn Gln Phe Arg Thr Cys Leu Ser
 85 90 95
 50 Cys Ser Ser Ser Cys Thr Thr Asp Gln Val Glu Ile Arg Ala Cys Thr
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 Lys Gln Gln Asn Arg Val Cys Ala Cys Glu Ala Gly Arg Tyr Cys Ala
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 55 Leu Lys Thr His Ser Gly Ser Cys Arg Gln Cys Met Arg Leu Ser Lys
 130 135 140
 60 Cys Gly Pro Gly Phe Gly Val Ala Ser Ser Arg Ala Pro Asn Gly Asn

145 150 155 160
 Val Leu Cys Lys Ala Cys Ala Pro Gly Thr Phe Ser Asp Thr Thr Ser
 165 170 175
 5 Ser Thr Asp Val Cys Arg Pro His Arg Ile Cys Ser Ile Leu Ala Ile
 180 185 190
 10 Pro Gly Asn Ala Ser Thr Asp Ala Val Cys Ala Pro Glu Ser Pro Thr
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 15 Arg Ser Gln
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 35 40 45
 35 Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
 50 55 60
 Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
 65 70 75 80
 40 Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
 85 90 95
 Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
 100 105 110
 45 Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
 115 120 125
 50 Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
 130 135 140
 Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
 145 150 155 160
 55 Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
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 Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
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30	Cys	Pro	Asp	His	Tyr	Tyr	Thr	Asp	Ser	Trp	His	Thr	Ser	Asp	Glu	Cys	
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Met Ala Leu Lys

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Val Leu Pro Leu His Arg Thr Val Leu Phe Ala Ala Ile Leu Phe Leu
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Gln Glu Phe Lys Asp Arg Ser Gly Asn Cys Val Leu Cys Lys Gln Cys
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25 gga cct ggc atg gag ttg tcc aag gaa tgt ggc ttc ggc tat ggg gag 307
Gly Pro Gly Met Glu Leu Ser Lys Glu Cys Gly Phe Gly Tyr Gly Glu
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30 gat gca cag tgt gtg ccc tgc agg ccg cac cgg ttc aag gaa gac tgg 355
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35 ggt ttc cag aag tgt aag cca tgt gcg gac tgt gcg ctg gtg aac cgc 403
Gly Phe Gln Lys Cys Lys Pro Cys Ala Asp Cys Ala Leu Val Asn Arg
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Phe Gln Arg Ala Asn Cys Ser His Thr Ser Asp Ala Val Cys Gly Asp
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Cys Leu Pro Gly Phe Tyr Arg Lys Thr Lys Leu Val Gly Phe Gln Asp
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Lys Glu Asp Trp Gly Phe Gln Lys Cys Lys Pro Cys Ala Asp Cys Ala
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20 Leu Val Asn Arg Phe Gln Arg Ala Asn Cys Ser His Thr Ser Asp Ala
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Val Cys Gly Asp Cys Leu Pro Gly Phe Tyr Arg Lys Thr Lys Leu Val
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 T; translated amino acid depends on genetic code

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 Met Asp Cys Gln Glu Asn Glu Tyr Trp Asp Gln
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55 tgg gga cgg tgt gtc acc tgc caa cgg tgt ggt cct gga cag gag cta 158
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 and 541 may be A, C, G, or T

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 25 tgg gga cgg tgt gtc acc tgc caa cgg tgt ggt cct gga cag gag cta 158
 Trp Gly Arg Cys Val Thr Cys Gln Arg Cys Gly Pro Gly Gln Glu Leu
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 Ser Lys Asp Cys Gly Tyr Gly Glu Gly Gly Asp Ala Tyr Cys Thr Ala
 30 35 40
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 Cys Pro Pro Arg Arg Tyr Lys Ser Ser Trp Gly His His Lys Cys Gln
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 agt tgc atc acc tgt gct gtc atc aat cgt gtt cag aag gtc caa ctg 302
 Ser Cys Ile Thr Cys Ala Val Ile Asn Arg Val Gln Lys Val Gln Leu
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 His Ser
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 ccccccaacn nctgnagggt ccaatgtggc cttncattt ggaagcttan tgggaaggca 478
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 Met Asp Cys Gln Glu Asn Glu Tyr Trp Asp Gln
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 tgg gga cgg tgt gtc acc tgc caa cgg tgt ggt cct gga cag gag cta 158
 Trp Gly Arg Cys Val Thr Cys Gln Arg Cys Gly Pro Gly Gln Glu Leu
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 Ser Lys Asp Cys Gly Tyr Gly Glu Gly Gly Asp Ala Tyr Cys Thr Ala
 30 35 , 40
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 tgc cct cct cgc agg tac aaa agc agc tgg ggc cac cac aaa tgt cag 254
 Cys Pro Pro Arg Arg Tyr Lys Ser Ser Trp Gly His His Lys Cys Gln
 45 50 55
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 agt tgc atc acc tgt gct gtc atc aat cgt gtt cag aag gtc aac tgc 302
 Ser Cys Ile Thr Cys Ala Val Ile Asn Arg Val Gln Lys Val Asn Cys
 60 65 70 75
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 aca gct acc tct aat gct gtc tgt ggg gac tgt ttg ccc agg ttc tac 350
 Thr Ala Thr Ser Asn Ala Val Cys Gly Asp Cys Leu Pro Arg Phe Tyr
 80 85 90
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 cga aag aca cgc att gga ggc ctg cag gac caa gag tgc atc ccg tgc 398
 Arg Lys Thr Arg Ile Gly Gly Leu Gln Asp Gln Glu Cys Ile Pro Cys
 95 100 105

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	Thr Lys Gln Thr Pro Thr Ser Glu Val Gln Cys Ala Phe Gln Leu Ser	
	110 115 120	
5	tta gtg gag gca gat gca ccc aca gtg ccc cct cag gag gcc aca ctt	494
	Leu Val Glu Ala Asp Ala Pro Thr Val Pro Pro Gln Glu Ala Thr Leu	
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	Val Ala Leu Val Ser Ser Leu Leu Val Val Phe Thr Leu Ala Phe Leu	
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	Gly Leu Phe Phe Leu Tyr Cys Lys Gln Phe Phe Asn Arg His Cys Gln	
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	cgt gga ggt ttg ctg cag ttt gag gct gat aaa aca gca aag gag gaa	638
	Arg Gly Gly Leu Leu Gln Phe Glu Ala Asp Lys Thr Ala Lys Glu Glu	
	175 180 185	
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	Ser Leu Phe Pro Val Pro Pro Ser Lys Glu Thr Ser Ala Glu Ser Gln	
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	Val Ser Trp Ala Pro Gly Ser Leu Ala Gln Leu Phe Ser Leu Asp Ser	
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	Val Pro Ile Pro Gln Gln Gln Gln Gly Pro Glu Met	
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	Tyr Gly Glu Gly Gly Asp Ala Tyr Cys Thr Ala Cys Pro Pro Arg Arg	
	35 40 45	
55	Tyr Lys Ser Ser Trp Gly His His Lys Cys Gln Ser Cys Ile Thr Cys	
	50 55 60	
60	Ala Val Ile Asn Arg Val Gln Lys Val Asn Cys Thr Ala Thr Ser Asn	
	65 70 75 80	

Ala Val Cys Gly Asp Cys Leu Pro Arg Phe Tyr Arg Lys Thr Arg Ile
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5 Gly Gly Leu Gln Asp Gln Glu Cys Ile Pro Cys Thr Lys Gln Thr Pro
100 105 110

Thr Ser Glu Val Gln Cys Ala Phe Gln Leu Ser Leu Val Glu Ala Asp
115 120 125

10 Ala Pro Thr Val Pro Pro Gln Glu Ala Thr Leu Val Ala Leu Val Ser
130 135 140

Ser Leu Leu Val Val Phe Thr Leu Ala Phe Leu Gly Leu Phe Phe Leu
145 150 155 160

15 Tyr Cys Lys Gln Phe Phe Asn Arg His Cys Gln Arg Gly Gly Leu Leu
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20 Gln Phe Glu Ala Asp Lys Thr Ala Lys Glu Glu Ser Leu Phe Pro Val
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Pro Pro Ser Lys Glu Thr Ser Ala Glu Ser Gln Val Ser Trp Ala Pro
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25 Gly Ser Leu Ala Gln Leu Phe Ser Leu Asp Ser Val Pro Ile Pro Gln
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Gln Gln Gln Gly Pro Glu Met
225 230

30